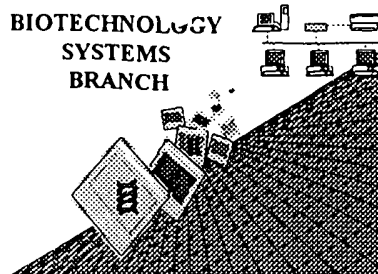


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/708,506
Source: Batch
Date Processed by STIC: 4-4-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/708,506

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of "Artificial" (NEW RULES) Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.
- 12 ☒ Use of <220>Feature (NEW RULES) Sequence(s) ☐ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

BATCH

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/708,506

DATE: 04/04/2001

TIME: 12:05:23

Input Set : A:\Merck256.app

Output Set: N:\CRF3\04042001\I708506.raw

Does Not Comply
Corrected Diskette Needed

See pp. 2-5

```

3 <110> APPLICANT: HARTMANN, ARNO
4   BRANDT, SILKE
5   RIEKE, ERWIN
6   SOBEL, CORNELIUS
7   LO, KIN-MING
8   WAY, JEFFREY C.
9   GILLIES, STEPHEN
11 <120> TITLE OF INVENTION: ERYTHROPOIETIN FORMS WITH IMPROVED PROPERTIES
13 <130> FILE REFERENCE: MERCK-2056
15 <140> CURRENT APPLICATION NUMBER: 09/708,506
16 <141> CURRENT FILING DATE: 2000-11-09
18 <150> PRIOR APPLICATION NUMBER: 60/164,855
19 <151> PRIOR FILING DATE: 1999-11-12
21 <160> NUMBER OF SEQ ID NOS: 26
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 514
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (8)..(505)
33 <223> OTHER INFORMATION: Human EPO, DNA sequence modified but no change in
34   protein sequence
36 <400> SEQUENCE: 1
37 cccgggt gcc cca cca cgc ctc atc tgt gac agc cga gtg ctg gag agg 49
38   Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg
39   1 5 10
41 tac ctc ttg gag gcc aag gag gcc gag aat atc acg acc ggc tgt gct 97
42 Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala
43 15 20 25 30
45 gaa cac tgc agc ttg aat gag aac atc acc gtg cct gac acc aaa gtg 145
46 Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val
47 35 40 45
49 aat ttc tat gcc tgg aag agg atg gag gtt ggc cag cag gcc gta gaa 193
50 Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu
51 50 55 60
53 gtg tgg cag ggc ctg gcc ctg ctg tcg gaa gct gtc ctg cgg ggc cag 241
54 Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln
55 65 70 75
57 gcc ctg ttg gtc aac tct tcc cag ccg tgg gag ccc ctg caa ctg cat 289
58 Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His
59 80 85 90
61 gtg gat aaa gcc gtg agt ggc ctt cgc agc ctc acc act ctg ctt cgg 337
62 Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg
63 95 100 105 110
65 gct ctg gga gcc cag aag gaa gcc atc tcc cct cca gat gcg gcc tca 385

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/708,506

DATE: 04/04/2001

TIME: 12:05:23

Input Set : A:\Merck256.app

Output Set: N:\CRF3\04042001\I708506.raw

```

66 Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser
67          115          120          125
69 gct gct ccc ctc cgc aca atc act gct gac act ttc cgc aaa ctc ttc   433
70 Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe
71          130          135          140
73 cga gtc tac tcc aat ttc ctc cgg gga aag ctg aag ctg tac aca ggg   481
74 Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly
75          145          150          155
77 gag gcc tgc cgg aca ggg gac aga tgactcgag   514
78 Glu Ala Cys Arg Thr Gly Asp Arg
79          160          165
82 <210> SEQ ID NO: 2
83 <211> LENGTH: 166
84 <212> TYPE: PRT
85 <213> ORGANISM: Homo sapiens
87 <400> SEQUENCE: 2
88 Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
89   1          5          10          15
91 Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
92          20          25          30
94 Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
95          35          40          45
97 Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
98   50          55          60
100 Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
101  65          70          75          80
103 Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
104          85          90          95
106 Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
107          100          105          110
109 Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
110          115          120          125
112 Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
113          130          135          140
115 Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
116 145          150          155          160
118 Cys Arg Thr Gly Asp Arg
119          165
123 <210> SEQ ID NO: 3
124 <211> LENGTH: 52
125 <212> TYPE: DNA
126 <213> ORGANISM: Artificial Sequence
128 <220> FEATURE:
129 <223> OTHER INFORMATION: Description of Artificial Sequence: Oligol
131 <400> SEQUENCE: 3
132 ccgggtgccc caccagcct catctgtgac agccgagtgc tggagaggtta cc   52
135 <210> SEQ ID NO: 4
136 <211> LENGTH: 49
137 <212> TYPE: DNA

```

What is the source of the genetic material in the sequence? See #12 on the Error Summary Sheet.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/708,506

DATE: 04/04/2001

TIME: 12:05:23

Input Set : A:\Merck256.app

Output Set: N:\CRF3\04042001\I708506.raw

138 <213> ORGANISM: Artificial Sequence
140 <220> FEATURE:
141 <223> OTHER INFORMATION: Description of Artificial Sequence: (Oligo2)
143 <400> SEQUENCE: 4
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147 <210> SEQ ID NO: 5
148 <211> LENGTH: 52
149 <212> TYPE: DNA
150 <213> ORGANISM: Artificial Sequence
152 <220> FEATURE:
153 <223> OTHER INFORMATION: Description of Artificial Sequence: (Oligo3)
155 <400> SEQUENCE: 5
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159 <210> SEQ ID NO: 6
160 <211> LENGTH: 48
161 <212> TYPE: DNA
162 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
165 <223> OTHER INFORMATION: Description of Artificial Sequence: (Oligo4)
167 <400> SEQUENCE: 6
168 gcctggaaga ggatggaggt tggccagcag gccgtagaag tgtggcag 48
171 <210> SEQ ID NO: 7
172 <211> LENGTH: 51
173 <212> TYPE: DNA
174 <213> ORGANISM: Artificial Sequence
176 <220> FEATURE:
177 <223> OTHER INFORMATION: Description of Artificial Sequence: (Oligo5)
179 <400> SEQUENCE: 7
180 ggcctggccc tgctgtcgga agctgtcctg cggggccagg ccctgttggt c 51
183 <210> SEQ ID NO: 8
184 <211> LENGTH: 49
185 <212> TYPE: DNA
186 <213> ORGANISM: Artificial Sequence
188 <220> FEATURE:
189 <223> OTHER INFORMATION: Description of Artificial Sequence: (Oligo6)
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195 <210> SEQ ID NO: 9
196 <211> LENGTH: 52
197 <212> TYPE: DNA
198 <213> ORGANISM: Artificial Sequence
200 <220> FEATURE:
201 <223> OTHER INFORMATION: Description of Artificial Sequence: (Oligo7)
203 <400> SEQUENCE: 9
204 tgagtggcct tcgcagcctc accactctgc ttcgggctct gggagcccag aa 52
207 <210> SEQ ID NO: 10
208 <211> LENGTH: 48
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence

see p.1

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/708,506

DATE: 04/04/2001

TIME: 12:05:23

Input Set : A:\Merck256.app

Output Set: N:\CRF3\04042001\I708506.raw

212 <220> FEATURE:
213 <223> OTHER INFORMATION: Description of Artificial Sequence: (Oligo8)
215 <400> SEQUENCE: 10
216 ggaagccatc tccccctccag atgcggcctc agctgctccc ctccgcac 48
219 <210> SEQ ID NO: 11
220 <211> LENGTH: 53
221 <212> TYPE: DNA
222 <213> ORGANISM: Artificial Sequence
224 <220> FEATURE:
225 <223> OTHER INFORMATION: Description of Artificial Sequence: (Oligo9)
227 <400> SEQUENCE: 11
228 aatcactgct gacactttcc gcaaactott ccgagtctac tccaatttcc tcc 53
231 <210> SEQ ID NO: 12
232 <211> LENGTH: 59
233 <212> TYPE: DNA
234 <213> ORGANISM: Artificial Sequence
236 <220> FEATURE:
237 <223> OTHER INFORMATION: Description of Artificial Sequence: (Oligo10)
239 <400> SEQUENCE: 12
240 ggggaaagct gaagctgtac acaggggagg cctgccggac aggggacaga tgactcgag 59
243 <210> SEQ ID NO: 13
244 <211> LENGTH: 49
245 <212> TYPE: DNA
246 <213> ORGANISM: Artificial Sequence
248 <220> FEATURE:
249 <223> OTHER INFORMATION: Description of Artificial Sequence: (Oligo11)
251 <400> SEQUENCE: 13
252 tcttgaggcc caaggaggcc gagcagatca cgaccggctg tgctgaaca 49
255 <210> SEQ ID NO: 14
256 <211> LENGTH: 52
257 <212> TYPE: DNA
258 <213> ORGANISM: Artificial Sequence
260 <220> FEATURE:
261 <223> OTHER INFORMATION: Description of Artificial Sequence: (Oligo12)
263 <400> SEQUENCE: 14
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267 <210> SEQ ID NO: 15
268 <211> LENGTH: 49
269 <212> TYPE: DNA
270 <213> ORGANISM: Artificial Sequence
272 <220> FEATURE:
273 <223> OTHER INFORMATION: Description of Artificial Sequence: (Oligo13)
275 <400> SEQUENCE: 15
276 cagtcttccc agccgtggga gcccctgcaa ctgcatgtgg ataaagccg 49
279 <210> SEQ ID NO: 16
280 <211> LENGTH: 48
281 <212> TYPE: DNA
282 <213> ORGANISM: Artificial Sequence
284 <220> FEATURE:

See p. 1

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/708,506

DATE: 04/04/2001

TIME: 12:05:23

Input Set : A:\Merck256.app

Output Set: N:\CRF3\04042001\I708506.raw

285 <223> OTHER INFORMATION: Description of Artificial Sequence, Oligo14 See p.1
 287 <400> SEQUENCE: 16
 288 ggaagccatc tcccctccag atgcggccgc agctgctccc ctccgcac 48
 291 <210> SEQ ID NO: 17
 292 <211> LENGTH: 232
 293 <212> TYPE: PRT
 294 <213> ORGANISM: Homo sapiens
 296 <220> FEATURE:
 297 <223> OTHER INFORMATION: Human IgG1 Fc region-mature protein
 299 <400> SEQUENCE: 17
 300 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 301 1 5 10 15
 303 Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 304 20 25 30
 306 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 307 35 40 45
 309 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 310 50 55 60
 312 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 313 65 70 75 80
 315 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 316 85 90 95
 318 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 319 100 105 110
 321 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 322 115 120 125
 324 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
 325 130 135 140
 327 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 328 145 150 155 160
 330 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 331 165 170 175
 333 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 334 180 185 190
 336 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 337 195 200 205
 339 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 340 210 215 220
 342 Ser Leu Ser Leu Ser Pro Gly Lys
 343 225 230
 346 <210> SEQ ID NO: 18
 347 <211> LENGTH: 326
 348 <212> TYPE: PRT
 349 <213> ORGANISM: Homo sapiens
 351 <220> FEATURE:
 352 <223> OTHER INFORMATION: Human IgG2 constant region (CH1, hinge, CH2,
 353 Ch3) - mature protein
 355 <400> SEQUENCE: 18
 356 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/708,506

DATE: 04/04/2001

TIME: 12:05:24

Input Set : A:\Merck256.app

Output Set: N:\CRF3\04042001\I708506.raw



Address: COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.

EXAMINER	
ART UNIT	PAPER NUMBER

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application.

Commissioner of Patents

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures.

APPLICANT IS GIVEN ONE EXTENDIBLE MONTH FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Direct the response to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to
whose telephone number is (703) 30

Application No.: 097085-06

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE